

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: January 15, 2003, 15:30:12 : Search time 7.28571 seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-18

Perfect score: 24
Sequence: 1 KEELM 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	95	GVPS_BACME	G68671 bacillus me
2	24	100.0	100.0	RL10_HELPJ	G2832 hellicobacte
3	24	100.0	164	RL10_HELPJ	P56036 hellicobacte
4	24	100.0	165	DEST_CHICK	P18359 gallus gall
5	24	100.0	165	DEST_HUMAN	P18202 homo sapien
6	24	100.0	165	DEST_MOUSE	G28055 mus musculu
7	24	100.0	167	CAPR_ATRNU	P41210 atriplex nu
8	24	100.0	168	VA34_VACCV	P41057 vaccinia vi
9	24	100.0	168	VA34_VACCV	P41057 vaccinia vi
10	24	100.0	168	VA34_VACCV	P41057 vaccinia vi
11	24	100.0	283	APMG_BRWCH	P26211 crwinia chr
12	24	100.0	291	APMG_BRWCH	P46737 mus musculu
13	24	100.0	312	APMG_BRWCH	P52215 rattus norv
14	24	100.0	316	Y014_HUMAN	P46736 homo sapien
15	24	100.0	316	Y014_MPTTA	G60349 methanococo
16	24	100.0	330	GAPP_SULAC	P39464 sulfolobus
17	24	100.0	434	CBPH_BOVIN	P04806 bos taurus
18	24	100.0	435	CBPH_MOUSE	P24544 mus musculu
19	24	100.0	446	CBPH_MOUSE	G29534 arabidopsi
20	24	100.0	448	KIM2_HUMAN	P44532 homo sapien
21	24	100.0	467	KIM6_HUMAN	G76013 homo sapien
22	24	100.0	476	CBPH_HUMAN	P16870 homo sapien
23	24	100.0	476	CBPH_MOUSE	G00493 mus musculu
24	24	100.0	476	CBPH_MOUSE	P15087 rattus norv
25	24	100.0	492	TIG_PHILO	G98168 rhizobium l
26	24	100.0	496	ML15_APATH	G00580 arabidopsi
27	24	100.0	526	IEG3_HSV7J	P52355 human herpe
28	24	100.0	526	ML15_APATH	G44621 arabidopsi
29	24	100.0	561	NCAP_PIARV	P03541 pichinde ar
30	24	100.0	576	MOHS_HUMAN	P26008 homo sapien
31	24	100.0	576	MOHS_HUMAN	P26041 mus musculu
32	24	100.0	576	MOHS_MOUSE	P26042 sus scrofa
33	24	100.0	580	E2R1_BOVIN	P31976 bos taurus

34	24	100.0	583	1	RADI_HUMAN	P45241 homo sapien
35	24	100.0	583	1	RADI_MOUSE	P26043 mus musculu
36	24	100.0	583	1	PAC1_PIG	P26044 sus scrofa
37	24	100.0	585	1	E2R1_HUMAN	P15311 homo sapien
38	24	100.0	585	1	E2R1_MOUSE	P26040 mus musculu
39	24	100.0	594	1	NC65_HUMAN	G00556 homo sapien
40	24	100.0	601	1	GLMS_PYRAE	G02120 p glucosami
41	24	100.0	605	1	E2R1_TREPA	P38746 trepanula p
42	24	100.0	647	1	KNRI_DROME	P13054 drosophila
43	24	100.0	670	1	DNLJ_HACST	G07703 bacillus st
44	24	100.0	721	1	DNAK_APHHA	G52960 aphanothece
45	24	100.0	868	1	AC02_SYNT3	P74562 synchocyst

ALIGNMENTS

RESULT 1			
GVPS_BACME	STANDARD:	PPT:	95 AA.
ID GVPS_BACME			
AC O68671;			
DI 15 JUN 2002 (Rel. 41, Created)			
DI 15 JUN 2002 (Rel. 41, Last sequence update)			
DI 15 JUN 2002 (Rel. 41, Last annotation update)			
DE Gas vesicle protein GvpS.			
GN GVPS.			
OS Bacillus megaterium.			
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX NCBI_taxonomy:1404;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN-VT1550;			
RA Medline:98233742; PubMed:9573198;			
RA Li N., Cannon M.C.;			
RT "Gas vesicle genes identified in Bacillus megaterium and functional			
RT expression in Escherichia coli."			
RL J. Bacteriol. 180:2450-2458(1998).			
CC - SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE A FAMILY.			
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CC or send an email to license@sib-sib.ch).			
CC EMBL: AF053765; AAC38410.1;			
CC InterPro: Ipp006038; Gas_vesicle			
CC Pfam: PF00741; Gas_vesicle; 1.			
CC TrEMBL: P006038; Gas_vesicle; 1.			
CC PROSITE: P50024; GAS_VESICLE_A.1; FALSE_NEG.			
CC PROSITE: P50024; GAS_VESICLE_A.2; FALSE_NEG.			
CC KW Gas vesicle.			
CC SEQUENCE 95 AA: 10422 MW: 10422 MW: AAFVAFEP2725603B CR064;			

Query Match			
Best local similarity: 100.0%, Score 24, DB 1, Length 95;			
Matches 5, Conservative 6, Mismatches 0, Indels 0, Gaps 0;			
QY	1 KEELM 5		
DB	76 KEELM 80		
RESULT 2			
RL10_HELPJ	STANDARD;	PRT;	164 AA.
DI 30 MAY 2000 (Rel. 39, Created)			
DI 30 MAY 2000 (Rel. 39, Last sequence update)			
DI 16 OCT 2001 (Rel. 40, Last annotation update)			
DE 50S ribosomal protein L10.			

GN RPL1 OR JH1123.
 OS Helicobacter pylori 399 (Campylobacter pylori 399).
 CC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 CC Helicobacter
 CC NCHI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed 9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.J., King R.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan R., Cull D.H.C., deJonghe R.L., Carmel G.,
 RA Lumino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Morberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
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 DR EMBL: AF001540; AA006701.1;
 DR InterPro: IPR001790; Ribosomal_L10.
 DR Pfam: PF004466; Ribosomal_L10; 1.
 DR PROSITE: PS01109; Ribosomal_L10; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 164 AA; 18573 MW; E307C2448B5F17F6 CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 132 KEELM 136
 RESULT 3
 ID R110_HELPY STANDARD; PRT; 164 AA.
 AC P56036;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein l10.
 GN RPL1 OR HP1200.
 OS Helicobacter pylori (Campylobacter pylori).
 CC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 CC Helicobacter.
 CC NCHI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=26695 / AFCC 700392;
 RX MEDLINE=97494467; PubMed=9252185;
 RA Tomb J.-F., White O., Kiehlman K.A., Klek H.-P., Gill S., Dougherty B.A.,
 RA Fleischmann R.D., Ketchum K.A., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson J., Dodson R., Khatak H.G., Glodek A.,
 RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Geyrhofer T.B., Unterbach T.E., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.B., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "the complete genome sequence of the gastric pathogen Helicobacter
 RT pylori.";
 RL Nature 398:539-547(1997).
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

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 DR EMBL: AF000626; AA008246.1;
 DR TIGR: HP1200;
 DR InterPro: IPR001790; Ribosomal_L10.
 DR InterPro: IPR002363; Ribosomal_L10eub.
 DR Pfam: PF004466; Ribosomal_L10; 1.
 DR PROSITE: PS01109; Ribosomal_L10; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 164 AA; 18605 MW; 9915415p78AF5D97 CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 132 KEELM 136
 RESULT 4
 ID DEST_CHICK STANDARD; PRT; 165 AA.
 AC P18359;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Destrin (Actin-depolymerizing factor) (ADP).
 GN DSTN OR DSN.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCHI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 101-111 AND 116-134.
 RC TISSUE=Brain;
 RX MEDLINE=91027754; PubMed=2223773;
 RA Adams M.E., Minamide I.S., Duester G., Hamburg J.R.;
 RT "Nucleotide sequence and expression of a cDNA encoding chick brain
 RT actin depolymerizing factor.";
 RL Biochemistry 29:7434-7439(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=91027755; PubMed=1699599;
 RA Abe H., Endo T., Yamamoto K., Ohinata T.;
 RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin
 RT of embryonic chicken skeletal muscle: two functionally distinct
 RT actin-regulatory proteins exhibit high structural homology.";
 RL Biochemistry 29:7420-7425(1990).
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-
 CC ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-
 CC INDEPENDENT MANNER.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS AND FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: J02912; AAA48575.1;
 DR EMBL: M55660; AAA48573.1;

DR PIR: A35702; A35702.
 DR PIR: A35703; A35703.
 DR HSP: P18282; 1AK6.
 DR InterPro: IPR002108; Actbind_cofin.
 DR Pfam: PF00241; cofilin_ADF_1.
 DR PRINTS: PR00006; COFILIN.
 DR ProDom: PD002129; Actbind_cofin; 1.
 DR SMART: SM0102; ADF; 1.
 DR PROSITE: PS00325; ACTIN-DEPOLYMERIZING; 1.
 KW Actin-binding.
 FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
 SQ SEQUENCE 165 AA; 18422 MW; 7699200245140629 CRC64;
 Query Match 100.0%, Score 24, DB 1, Length 165.
 Best Local Similarity: 100.0%, Pred. No. 54.
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KEELM 5
 DB 96 KEELM 100
 RESULT 5
 DEST_HUMAN STANDARD; PRT; 165 AA.
 AC P18282;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Destrin (Actin-depolymerizing factor) (ADF).
 GN DSTN OR DSN OR ACTDP.
 OS Homo sapiens (Human), and
 OS Sus scrofa (Pig).
 OC Eukaryota, Metazoa, Chordata, Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria, Primates; Catarrhini, Hominoidea, Homo.
 OX NCBI_TaxID=9606, 9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human; TISSUE-Brain;
 RX MEDLINE=9400200q; PubMed=8369167;
 RA Hawkins M., Pope R., Maciver S K., Woods A G;
 RT "Human actin depolymerizing factor mediates a pH-sensitive
 destruction of actin filaments."
 RL Biochemistry 32:9085-9093(1993)
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE=2163749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Barton J., Gilbert J.G.R.,
 RA Jones M., Starikov G., Almeida J.P., Babington A.K., Bagdikian C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley G.P., Bird C.F., Blake S.E., Bridgman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.T., Deadman P., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam P., Hall P.E.,
 RA Hammond S., Harley J., Heath P.D., Ho S., Holden J., Howden P.J.,
 RA Huckle E., Hunter A.R., Hunt S.E., Jokusch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,
 RA Lehtavirta M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell T.D.,
 RA Marsh V.L., Martin S.L., McConachie I.T., Melay C.A., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,
 RA Phillimore R.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.F., Shih H.K., Showkjee P., Sims S.,
 RA Skuce C.D., Smith M.I., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromas A.C., Vaudin M., Wall M., Wallis T.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams F., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414 865-871(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human; TISSUE-lung;
 RA Strausberg R.;
 RL Submitted (JUN 2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.; AND SEQUENCE OF 53-69 AND 96-112.
 RC SPECIES-Pig; TISSUE-Brain;
 RX MEDLINE=96203224; PubMed=215828;
 RA Moriyama K., Nishida F., Yamaguchi N., Sakai H., Matsumoto S.,
 RA Iida K., Yahara I.;
 RT "Destrin, a mammalian actin depolymerizing protein, is closely
 related to cofilin. Cloning and expression of porcine brain destrin
 cDNA.";
 RL J. Biol. Chem. 265:5768-5773(1990).
 RN [5]
 RP STRUCTURE BY NMR.
 RC SPECIES-Pig;
 RX MEDLINE=96270507; PubMed=8674111;
 RA Hatanaka H., Ogura K., Moriyama K., Ichikawa S., Yahara I.,
 RA Inagaki F.;
 RT "Tertiary structure of destrin and structural similarity between two
 actin-regulating protein families.";
 RL Cell 85:1047-1055(1996).
 CC -!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-
 ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-
 INDEPENDENT MANNER.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.
 CC -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S65738; AAB29361.1; -;
 DR EMBL: AL142765; CAC10585.1; -;
 DR EMBL: BC009477; AA09477.1; -;
 DR EMBL: D90953; BAA14105.1; -;
 DR PIR: A35179; A35179.
 DR PIR: A54184; A54184.
 DR PDB: 1AK6; 12-NOV-97.
 DR PDB: 1AK7; 15-OCT-97.
 DR Genbank: M2N15750; DSTN.
 DR InterPro: IPR002108; Actbind_cofin.
 DR Pfam: PF00241; cofilin_ADF_1.
 DR PRINTS: PR00006; COFILIN.
 DR ProDom: PD002129; Actbind_cofin; 1.
 DR SMART: SM0102; ADF; 1.
 DR PROSITE: PS00325; ACTIN-DEPOLYMERIZING; 1.
 KW Actin-binding; 3D-structure. NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 30 34
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
 SQ SEQUENCE 165 AA; 18506 MW; 89684167924100E CRC64;
 Query Match 100.0%, Score 24, DB 1, Length 165.
 Best Local Similarity: 100.0%, Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KEELM 5
 DB 96 KEELM 100
 RESULT 6
 DEST_MOUSE STANDARD; PRT; 165 AA.
 ID TEST_MOUSE

Q9R0P5;
 16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 Deslrin (Actin-depolymerizing factor) (ADF).
 OSIN OR DSN OR SIDA;
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 Soki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Saito T.;
 "Mouse actin depolymerizing factor sda23";
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-
 INDEPENDENT MANNER.
 -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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 EMBL; AB025406; BAA84691.1;
 RSDP; P18282; IAK6
 MCD; M61:1924270; Dstn.
 InterPro: IPR002108; Actbind_cofin.
 Pfam: PF00241; Colilin_ADF; 1.
 PRINTS: PR00006; COFILIN.
 ProDom: PD002129; Actbind_cofin; 1.
 SMART: SM00102; ADF; 1.
 PROSITE: PS00125; ACTIN_DEPOLYMERIZING; 1.
 Actin-binding.
 KW DOMAIN 40 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).
 SQ SEQUENCE 165 AA; 18521 MW; 42R0076469B4667 CP*64;
 Query Match 100.0%; Score 24; DH 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 96 KEELM 100
 [1]
 RESULT 7
 CATR_ATRNO STANDARD; PRT; 167 AA.
 ID CATR_ATRNO
 AC P41210;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 41, Last sequence update)
 DT 01-Nov-1995 (Rel. 42, Last annotation update)
 DE Caltractin (centrin).
 OS Atriplex nummularia.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Caryophyllales; Cistaceaceae; Atriplex.
 NCBI_TaxID=4554;
 [1]
 SEQUENCE FROM N.A.
 Zhu J., K., Bressan R.A., Hasegawa P.M.;
 "An Atriplex nummularia cDNA with sequence relatedness to the algal caltractin gene".
 Plant Physiol. 99:1734-1745(1992).
 -1- FUNCTION: PLAYS A FUNDAMENTAL ROLE IN MICROTUBULE-ORGANIZING
 CENTER STRUCTURE AND FUNCTION.
 -1- SUBCELLULAR LOCATION: CYTOSOL; SOME OF INTERPHASE AND MITOTIC CELLS.

-1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BELONGS
 THE CALTRACTIN/CDC31 SUBFAMILY.
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 EMBL; M90970; ?; NOT_ANNOTATED_CDS.
 HSSP; P02593; ICDM.
 InterPro: IPR002048; EF-hand.
 Pfam: PF00036; efhand; 4;
 ProDom: PD000012; EF-hand; 2.
 SMART: SM00054; EFH; 4.
 PROSITE: PS00018; EF_HAND; 4.
 KW Calcium-binding; Repeat; Cell division; Mitosis.
 FT CA_BIND 35 46 EF-HAND 1 (PROBABILE).
 FT CA_BIND 71 82 EF-HAND 2 (PROBABILE).
 FT CA_BIND 108 119 EF-HAND 3 (PROBABILE).
 FT CA_BIND 144 155 EF-HAND 4 (PROBABILE).
 SQ SEQUENCE 167 AA; 19244 MW; 3A2D0AC6956HHD6C CRC64;
 Query Match 100.0%; Score 24; DH 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 97 KEELM 101
 [1]
 RESULT 8
 VA34_VACCC STANDARD; PRT; 168 AA.
 ID VA34_VACCC
 AC P21057;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein A34.
 CN A34R.
 OS Vaccinia virus (strain Copenhagen).
 OR Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 Orthopoxvirus.
 NCBI_TaxID=10249;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91021027; PubMed-2219722;
 RA Goebel S T, Johnson G P, Perkus M E, Davis S W, Winslow J P, Paoletti E;
 "The complete DNA sequence of vaccinia virus.";
 Virolgy 179:247-266(1990).
 RN [2]
 RP COMPLETE GENOME.
 RA Goebel S T, Johnson G P, Perkus M E, Davis S W, Winslow J P, Paoletti E;
 "Appendix to 'The complete DNA sequence of vaccinia virus.'";
 Virolgy 179:517-563(1990).
 CC -1- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED
 VIRUS AND GROSS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.
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 EMBL; M15027; AAA48161.1;
 PIR; 14520; 142520.

DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; Lectin_C; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.
 KW Transmembrane.
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.
 FT DOMAIN 21 168 EXTRACELLULAR
 SQ SEQUENCE 168 AA: 19555 MW: 32928480.140255 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;
 Best Local Similarity 100.0%; Pfam No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 39 KEELM 43

RESULT 9
 VA34_VACCV STANDARD; PRT; 168 AA.
 AC P24761;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Protein A34.
 GN A34R OR SALIAR.
 OS Vaccinia virus (strain WR).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus
 OX NCBI_TaxID=10254;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91259063; PubMed=2045793;
 RA Smith G.L., Chan Y.S., Howard S.T.,
 RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WP from near
 the right inverted terminal repeat.";
 PL J. Gen. Virol. 72:1349-1376(1991).
 RN [2]

RP COMPLETE GENOME.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=9320281; PubMed=8384129;
 RA Shchelkunov S.N., Matcenikova S.S., Totmenin A.V., Blinov V.M.,
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 CC -!- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED
 CC VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.
 CC (BY SIMILARITY).

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 CC -----

DR EMRL: D11079; BAA01804.1;
 DR EMRL: M61187; AAA48331.1;
 DR EMRL: A19583; CAA01480.1;
 DR PIR: TQ1770; TQ1770
 DR InterPro: IPR001304; Lectin_C
 DR Pfam: PF00059; Lectin_C; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.

KW Transmembrane.
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.
 FT DOMAIN 21 168 EXTRACELLULAR
 SQ SEQUENCE 168 AA: 19555 MW: 69F72EA9D971F19F CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;
 Best Local Similarity 100.0%; Pfam No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 39 KEELM 43

RESULT 10
 VA34_VAFV STANDARD; PRT; 168 AA.
 AC P33851;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Protein A34.
 GN A34R OR A37R.
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus
 OX NCBI_TaxID=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=92209372; PubMed=1666548;
 RA Shchelkunov S.N., Matcenikova S.S., Totmenin A.V., Blinov V.M.,
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 CC -!- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED
 CC VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.
 CC (BY SIMILARITY).

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 CC -----

DR EMRL: X64198; CAA49082.1;
 DR EMRL: X61115; CAA47508.1;
 DR PIR: P35852; B36852.
 DR PIR: S46864; S46864.
 DR InterPro: IPR001304; Lectin_C
 DR Pfam: PF00059; Lectin_C; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00041; C_TYPE_LLECTIN_2; 1.

KW Transmembrane.
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.
 FT DOMAIN 21 168 EXTRACELLULAR
 SQ SEQUENCE 168 AA: 19611 MW: 28A8FDF95FA09634 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;
 Best Local Similarity 100.0%; Pfam No. 55;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 39 KEELM 43

RESULT 11
 ARBG_ERWCH

```

ID ARBO_PFWCH STANDARD: PRT: 283 AA.
AC P26211;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE beta-glucosidase operon antiterminator.
GN ARBO.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID-556;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92121114; PubMed-1732212;
RA el Hassouni M., Benissat B., Chippaux M., Barras F.;
RT "Nucleotide sequences of the arb genes, which control beta-glucoside
RT utilization in Erwinia chrysanthemi: comparison with the Escherichia
RT coli ba operon and evidence for a new beta-glycosylase family
RT including enzymes from eubacteria, archaeobacteria, and humans.";
RL J. Bacteriol. 174:765-777(1992).
CC -!- FUNCTION: MEDIATES THE POSITIVE REGULATION OF THE BETA-GLUCOSIDE
CC (ARB) OPERON BY FUNCTIONING AS A TRANSCRIPTIONAL ANTITERMINATOR
CC THIS IS A RNA-BINDING PROTEIN THAT RECOGNIZES A SPECIFIC SEQUENCE
CC LOCATED JUST UPSTREAM OF TWO TERMINATION SITES WITHIN THE OPERON
CC (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED AND INACTIVATED BY ARRF (11-HCL). THE DEGREE
CC OF PHOSPHORYLATION IS DEPENDENT ON THE PRESENCE OR ABSENCE OF
CC BETA-GLUCOSIDES WHICH ACT AS INDUCERS OF THE OPERON EXPRESSION.
CC ADDITION OF INDUCER RESULT IN THE RAPID DEPHOSPHORYLATION OF ARRG
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRANSCRIPTIONAL ANTITERMINATOR HCIG
CC FAMILY.
CC -----
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CC -----
DR EMBL: M81772; AAA24813.1; -
DR PIR: A42603; A42603
DR RSBP: J15401; 1A00
DR InterPro: IPR001550; BglG_antitermin.
DR InterPro: IPR004441; CAT_PRO.
DR Pfam: PF00874; BglG_antitermin; 2.
DR Pfam: PF03123; CAT_RBD; 1.
DR PROSITE: PS00654; ANTITERMINATORS_HCIG; 1.
KW Transcription regulation, Activator, RNA binding, Phosphorylation.
SQ SEQUENCE 283 AA; 33620 MW; A58VADRGGRHIA4K RPO64;

Query Match 100.0%; Score 24; DB 1; Length 283;
Best local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
Db 260 KEELM 264
|||||

RESULT 12
C61A_MOUSE STANDARD: PRT: 291 AA.
AC P46737; Q9D025;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C6.1A protein.
GN C6.1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94067776; PubMed-8247530;
RA Fisch P., Forster A., Sherrington P.D., Dyer M.J.S., Rabbitts T.H.;
RT "The chromosomal translocation t(X;14)(q28;q11) in T-cell pro-
RT lymphocytic leukaemia breaks within one gene and activates another.";
RL Oncogene 8:3271-3276(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57H1/6J; TISSUE=Embryo;
RX MEDLINE-21085660; PubMed 11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adachi T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasakawa I., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King H., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole C., Quackenbush J.,
RA Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bolunda N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nerdes P., Ping B., Pingwald M., Podriqez L., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Watz K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Horris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2002) to the FMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PSMD7/C6.1A FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S68022; AAR29006.2; -
DR EMBL: AK011876; BAH27894.1; -
DR EMBL: BC021313; AAH21313.1; -
DR InterPro: IPR000555; Mov34.
DR Pfam: PF01398; Mov34; 1.
DR Trdbom: T0004392; Mov34_1; 1.
DR SMART: SM00232; JAH_MFN; 1.
DR CONFLICT 280 280 K -> R (IN REF. 2).
SQ SEQUENCE 291 AA; 33540 MW; 82D18B79D8EC5F72 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 291;
Best local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
Db 280 KEELM 284
|||||

RESULT 13
ICE2_RAT STANDARD: PRT: 312 AA.
ID ICE2_RAT
AC P55215; O35398;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

```

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22. -) (CASP 2) (ICH-1 protease)
 DE (Fragment).
 GN CASP2 OR ICH1
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN 111
 RP SOURCE OF 1-257 FROM N.A.
 RC TISSUE-Kidney cortex;
 RX MEDLINE=98191709; PubMed=9540276;
 RA Kaushal G.P., Singh A.B., Shah S.V.;
 RT Identification of gene family of caspases in rat kidney and altered
 RT expression in ischemia-reperfusion injury.*;
 PL Am J Physiol 274:F587-F595(1998)
 PL 121
 RP SEQUENCE OF 131-312 FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=96042508; PubMed=7588240;
 RA Flaws J.A., Kugu K., Tibbovich A.M., Dasan A., Tilly K.;
 RA Hirshfield A.N., Tilly J.L.;
 RT Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
 RT endonuclease activity from morphological apoptosis in granulosa cells
 RT of the ovarian follicle.*;
 RL Endocrinology 136:5042-5053(1995)
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
 CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
 CC SIMILARITY).
 CC -1- PTM: THE MAJORITY PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
 CC THAT OF OTHER CASPASES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN
 CC
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 CC
 DR EMBL: AF025671; AAB2567.1; -;
 DR EMBL: U34684; AAB50260.1; -;
 DR HSP: P29466; LICE.
 DR MEROPS: C14.006; -;
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002398; ICE.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00115; CARD; 1.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1
 KW Hydrolyase, Thiol, Protease, AP-4tholase, Cysteine,
 FT NON_TER 1 1
 FT CHAIN <1 266 CASPASE-2 SUBUNIT P18 (BY SIMILARITY)
 FT CHAIN 267 >312 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
 FT CHAIN 281 >312 CASPASE-2 SUBUNIT P12 (BY SIMILARITY)
 FT DOMAIN <1 55 CARD.
 FT ACT_SITE 210 210 BY SIMILARITY.
 FT ACT_SITE 253 253 BY SIMILARITY.
 FT NON_TER 312 312
 SQ SEQUENCE 312 AA: 35070 MW: 318A0746212F9646 P06F4;

Query Match 100.0%, Score 24, DB 1, Length 312;
 Best Local Similarity 100.0%, Prod. No. 1e-02;
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 KEELM 5
 DB 283 KEELM 287

RESULT 14
 C61A_HUMAN STANDARD: PRT: 316 AA.
 AC P4746, EMP127, G16107,
 DT 01 NOV 1995 (Rel. 32, Created)
 DT 15 JUN 2002 (Rel. 41, Last sequence update)
 DT 15 JUN 2002 (Rel. 41, Last annotation update)
 DE C6.1A protein.
 GN C6.1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Placenta;
 RX MEDLINE=94265009; PubMed=1303175;
 RA Kenwick S., Levinson B., Taylor S., Shapiro A., Gitschier J.;
 RT Isolation and sequence of two genes associated with a CpG island 5'
 RT of the factor VIII gene.*;
 PL Hum Mol Genet 1:179-186(1992)
 RN 121
 RP SEQUENCE FROM N.A. (ISOFORM 2). AND CHROMOSOMAL TRANSLOCATION.
 RX MEDLINE=94057776; PubMed=8247530;
 RA Fisch P., Forster A., Sherrington P.D., Dyer M.J.S., Rabbitts T.H.;
 RT The chromosomal translocation t(X;14)(q28;q11) in T cell pro-
 RT lymphocytic leukaemia breaks within one gene and activates another.*;
 RN 131
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-lung;
 RA Strausberg R.;
 PL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 and 2 (shown here); are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal
 CC muscle, kidney and pancreas.
 CC -1- DISEASE: A form of pre-lymphocytic t-cell leukemia (T-PLL) is
 CC characterized by a chromosomal translocation t(X;14)(q28;q11)
 CC that involves C6.1A and T-cell receptor alpha chain (TCRA)
 CC genes.
 CC -1- SIMILARITY: BELONGS TO THE PSMD7/C6.1A FAMILY.
 CC
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 CC
 DR EMBL: X64643; CAA45917.1; -;
 DR EMBL: S68015; AAB29005.2; ALL_INIT.
 DR EMBL: X7002599; AAB2599.1; -;
 DR EMBL: BC000540; AAB06540.1; -;
 DR InterPro: IPR000555; Mov14
 DR Pfam: PF01398; Mov34; 1.
 DR ProDom: PD04402; Mov34.1; 1.
 DR SMART: SM00232; JAB.MPN; 1.
 KW Photo oncogene, Chromosomal translocation, Alternative splicing.
 FT VAR_SINGLE 184 208 MISSING (IN ISOFORM 1).
 FT CONFLICT 225 225 G S W (IN REF. 2).
 FT SEQUENCE 316 AA: 76092 MW: 57233SGLAIF7421 P0664;

Query Match 100.0%; Score 24; DH 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 305 KEELM 309

RESULT 15

Y014_METJA STANDARD; PRT; 316 AA.
 AC G60349;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0034.
 GN MJ0034.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID-2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE-9633799; PubMed-8688087;
 RA Bull C.J., White O., Olsen G.T., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Overbeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Goodbagon N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley T.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Kleuk H.P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RI Science 273:1058-1073(1996).

CC -f- SIMILARITY: BELONGS TO THE UPF0051 (YCF24) FAMILY.
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DR EMBL; U67462; AAB98015.1;
 DR TIGR; MJ0034;
 DR InterPro; IPR000825; UPF0051.
 DR Pfam; PF01458; UPF0051; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 316 AA; 35021 MW; 3657AC25CHE473D1 CRC64;

Query Match 100.0%; Score 24; DH 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
 DB 4 KEELM 8

Search completed: January 16, 2003, 16:51:10
 Job time : 8.28571 secs